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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/911,969

DATE: 02/07/2002
TIME: 17:32:58

Input Set : N:\Crf3\RULE60\09911969.txt
Output Set: N:\CRF3\02072002\I911969.raw

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:
7 (i) APPLICANT: Kawamura, Yukio; Morita,
8 Akihiro; Izumo, Koji.; Saka, Tomohide.
10 (ii) TITLE OF INVENTION: ANTITUMOR PROTEIN AND
11 GENE ENCODING SAME
13 (iii) NUMBER OF SEQUENCES: 20
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
17 (B) STREET: 345 PARK AVENUE
18 (C) CITY: NEW YORK
19 (D) STATE: NEW YORK
20 (E) COUNTRY: USA
21 (F) ZIP: 10154
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: FLOPPY DISK
25 (B) COMPUTER: IBM PC COMPATIBLE
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: MICROSOFT WORD 97
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/911,969
C--> 31 (B) FILING DATE: 24-Jul-2001
33 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 09/023,731
36 (B) FILING DATE: 13-FEB-1998
38 (A) APPLICATION NUMBER: JP 29275/1997
39 (B) FILING DATE: 13-FEB-1997
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: KENNETH H. SONNENFELD
43 (B) REGISTRATION NUMBER: 33,285
44 (C) REFERENCE/DOCKET NUMBER: 3479-4000
46 (ix) TELECOMMUNICATION INFORMATION:
47 (A) TELEPHONE: (212) 758-4800
48 (B) TELEFAX: (212) 751-6849
49 (C) TELEX: 421792
51 (2) INFORMATION FOR SEQ ID NO: 1:
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 566
55 (B) TYPE: amino acid
56 (D) TOPOLOGY: linear
58 (ii) MOLECULE TYPE: protein
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
62 Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg

ENTERED

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63	1	5	10	15												
65	Ser	Gln	Gly	Asp	Leu	Thr	Ser	Ser	Gln	His	Glu	Ile	Val	His	Phe	Thr
66					20				25				30			
67	Asp	Val	Phe	Ile	Ala	Gly	Ser	Gly	Pro	Ile	Ser	Cys	Thr	Tyr	Ala	Arg
68					35				40				45			
69	His	Ile	Ile	Asp	Asn	Thr	Ser	Thr	Thr	Lys	Val	Tyr	Met	Ala	Glu	Ile
70					50				55				60			
71	Gly	Ser	Gln	Asp	Asn	Pro	Val	Ile	Gly	Ala	His	His	Lys	Asn	Ser	Ile
72					65				70				75			80
73	Lys	Phe	Gln	Lys	Asp	Ile	Asp	Lys	Phe	Val	Asn	Ile	Ile	Asn	Gly	Ala
74					85				90				95			
75	Leu	Gln	Pro	Ile	Ser	Ile	Ser	Pro	Ser	Asp	Thr	Tyr	Gln	Pro	Thr	Leu
76					100				105				110			
77	Ala	Val	Ala	Ala	Trp	Ala	Pro	Pro	Ile	Asp	Pro	Ala	Glu	Gly	Gln	Leu
78					115				120				125			
79	Val	Ile	Met	Gly	His	Asn	Pro	Asn	Gln	Glu	Ala	Gly	Leu	Asn	Leu	Pro
80					130				135				140			
81	Gly	Ser	Ala	Val	Thr	Arg	Thr	Val	Gly	Gly	Met	Ala	Thr	His	Trp	Thr
82					145				150				155			160
83	Cys	Ala	Cys	Pro	Thr	Pro	His	Asp	Glu	Glu	Arg	Val	Asn	Asn	Pro	Val
84					165				170				175			
85	Asp	Lys	Gln	Glu	Phe	Asp	Ala	Leu	Leu	Glu	Arg	Ala	Lys	Thr	Leu	Leu
86					180				185				190			
87	Asn	Val	His	Ser	Asp	Gln	Tyr	Asp	Asp	Ser	Ile	Arg	Gln	Ile	Val	Val
88					195				200				205			
89	Lys	Glu	Thr	Leu	Gln	Gln	Thr	Leu	Asp	Ala	Ser	Arg	Gly	Val	Thr	Thr
90					210				215				220			
91	Leu	Pro	Leu	Gly	Val	Glu	Arg	Arg	Thr	Asp	Asn	Pro	Ile	Tyr	Val	Thr
92					225				230				235			240
93	Trp	Thr	Gly	Ala	Asp	Thr	Val	Leu	Gly	Asp	Val	Pro	Lys	Ser	Pro	Arg
94					245				250				255			
95	Phe	Ala	Leu	Val	Thr	Glu	Thr	Arg	Val	Thr	Lys	Leu	Ile	Val	Ser	Glu
96					260				265				270			
97	Thr	Asn	Pro	Thr	Gln	Val	Val	Ala	Ala	Leu	Leu	Arg	Asn	Leu	Asn	Thr
98					275				280				285			
99	Ser	Asn	Asp	Glu	Leu	Val	Val	Ala	Lys	Ser	Phe	Val	Ile	Ala	Cys	Gly
100					290				295				300			
101	Ala	Val	Cys	Thr	Pro	Gln	Ile	Leu	Trp	Asn	Ser	Asn	Ile	Arg	Pro	Tyr
102					305				310				315			320
103	Ala	Leu	Gly	Arg	Tyr	Leu	Ser	Glu	Gln	Ser	Met	Thr	Phe	Cys	Gln	Ile
104					325				330				335			
105	Val	Leu	Lys	Arg	Gly	Ile	Val	Asp	Ala	Ile	Ala	Thr	Asp	Pro	Arg	Phe
106					340				345				350			
107	Ala	Ala	Lys	Val	Glu	Ala	His	Lys	Lys	Lys	His	Pro	Asp	Asp	Val	Leu
108					355				360				365			
109	Pro	Ile	Pro	Phe	His	Glu	Pro	Glu	Pro	Gln	Val	Met	Ile	Pro	Tyr	Thr
110					370				375				380			
111	Ser	Asp	Phe	Pro	Trp	His	Val	Gln	Val	His	Arg	Asp	Ala	Phe	Ser	Tyr
112					385				390				395			400

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113 Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg
114 405 410 415
115 Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly
116 420 425 430
117 Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr
118 435 440 445
119 Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly
120 450 455 460
122 Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met
123 465 470 475 480
124 Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly
125 485 490 495
126 Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln
127 500 505 510
128 Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu
129 515 520 525
130 Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro
131 530 535 540
132 Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val
133 545 550 555 560
134 Asn Tyr Leu Gly Val Ser
135 565

138 (2) INFORMATION FOR SEQ ID NO: 2:

140 (i) SEQUENCE CHARACTERISTICS:

141 (A) LENGTH: 1701

142 (B) TYPE: nucleic acid

C--> 143 (D) TOPOLOGY: linear

144 (D) STRANNESS: Single

146 (ii) MOLECULE TYPE: cDNA to RNA

148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

150 ATG CCG ATA CGT CTT TCC AAA GAA AAA ATC AAC GAC CTG CTG CAA CGT48

151 Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg

152 1 5 10 15

154 TCT CAA GGG GAT CTT ACT TCC TCG CAA CAC GAA ATT GTA CAT TTC ACT96

155 Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr

156 20 25 30

158 GAT GTT TTC ATT GCT GGC AGT GGT CCC ATT AGC TGT ACT TAC GCC CGC144

159 Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg

160 35 40 45

162 CAC ATC ATT GAC AAT ACC TCA ACT ACA AAG GTT TAC ATG GCC GAA ATA192

163 His Ile Ile Asp Asn Thr Ser Thr Lys Val Tyr Met Ala Glu Ile

164 50 55 60

166 GGT TCT CAA GAT AAC CCT GTC ATC GGG GCC CAT CAC AAG AAC TCC ATA240

167 Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile

168 65 70 75 80

170 AAG TTT CAG AAA GAC ATT GAC AAG TTT GTG AAT ATC ATC AAC GGT GCC288

171 Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala

172 85 90 95

174 CTC CAG CCG ATT TCG ATT TCG CCA TCG GAC ACC TAC CAG CCC ACT CTC336

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Input Set : N:\Crf3\RULE60\09911969.txt
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175 Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu
 176 100 105 110
 179 GCT GTA GCA GCG TGG GCG CCG CCC ATC GAT CCT GCC GAA GGC CAG CTC384
 180 Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu
 181 115 120 125
 183 GTG ATT ATG GGA CAC AAT CCG AAT CAG GAG GCC GGC CTG AAC CTT CCC432
 184 Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro
 185 130 135 140
 187 GGT AGC GCT GTC ACT AGG ACA GTC GGG GGG ATG GCG ACC CAC TGG ACT480
 188 Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr
 189 145 150 155 160
 191 TGC GCG TGT CCT ACT CCA CAT GAC GAA GAG AGG GTC AAC AAC CCA GTT528
 192 Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val
 193 165 170 175
 195 GAC AAG CAG GAG TTC GAC GCA CTG CTC GAA CGT GCT AAA ACA TTG CTC576
 196 Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu
 197 180 185 190
 199 AAC GTT CAC AGC GAC CAG TAC GAC GAT TCT ATC CGT CAG ATA GTT GTC624
 200 Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val
 201 195 200 205
 203 AAA GAG ACT CTT CAG CAG ACC CTT GAT GCG TCG CGG GGT GTG ACC ACT672
 204 Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr
 205 210 215 220
 207 CTC CCG CTG GGG GTG GAG CGC CGT ACG GAC AAT CCT ATT TAT GTC ACC720
 208 Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr
 209 225 230 235 240
 211 TGG ACC GGT GCC GAT ACC GTC CTT GGT GAT GTG CCG AAG AGT CCC CGA768
 212 Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg
 213 245 250 255
 215 TTC GCT TTG GTT ACA GAG ACG AGA GTG ACG AAG CTT ATT GTC AGT GAA816
 216 Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu
 217 260 265 270
 219 ACC AAT CCG ACG CAG GTT GCT GCG TTG CTA CGT AAC TTG AAT ACA864
 220 Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr
 221 275 280 285
 223 AGC AAC GAT GAA CTT GTC GTG GCC AAG AGT TTC GTC ATA GCT TGT GGA912
 224 Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly
 225 290 295 300
 227 GCA GTC TGC ACA CCG CAA ATC TTG TGG AAC AGC AAC ATC CGC CCA TAT960
 228 Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr
 229 305 310 315 320
 231 GCG CTT GGT CGC TAC CTC AGC GAA CAG TCC ATG ACT TTT TGT CAG ATC1008
 232 Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile
 233 325 330 335
 236 GTT CTC AAG AGG GGC ATA GTC GAT GCC ATC GCT ACT GAC CCT CGC TTC1056
 237 Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe
 238 340 345 350
 240 GCT GCG AAG GTT GAG GCG CAC AAG AAG CAC CCC GAT GAC GTG CTG1104
 241 Ala Ala Lys Val Glu Ala His Lys Lys His Pro Asp Asp Val Leu

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Input Set : N:\Crf3\RULE60\09911969.txt
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242 355 360 365
 244 CCC ATT CCA TTC CAC GAG CCT GAA CCT CAA GTG ATG ATT CCG TAC ACG1152
 245 Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr
 246 370 375 380
 248 TCG GAC TTC CCT TGG CAT GTC CAG GTG CAT CGC GAT GCA TTC TCA TAT1200
 249 Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr
 250 385 390 395 400
 252 GGT GAT GTT GGA CCC AAG GCC GAC CCG CGT GTT GTC GTC GAT CTG AGG1248
 253 Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg
 254 405 410 415
 256 TTT TTC GGC AAA TCA GAT ATT GTC GAA GAA AAT CGA GTG ACT TTC GGT1296
 257 Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly
 258 420 425 430
 260 CCG AAC CCT AAG CTA CGC GAG TGG GAA GCG GGT GTT ACA GAC ACT TAT1344
 261 Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr
 262 435 440 445
 264 GGA ATG CCA CAG CCG ACA TTC CAT GTC AAG CGG ACC AAC GCC GAT GGA1392
 265 Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly
 266 450 455 460
 268 GAC CGT GAC CAG AGG ATG ATG AAT GAT ATG ACC AAC GTC GCG AAC ATG1440
 269 Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met
 270 465 470 475 480
 272 CTG GGT GGG TAC CTT CCT GGC TCC TAC CCT CAA TTT ATG GCA CCT GGT1488
 273 Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly
 274 485 490 495
 276 CTC GTA CTG CAC ATC ACG GGA ACT ACT CGG ATC GGG ACA GAT GAT CAA1536
 277 Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln
 278 500 505 510
 280 ACT TCT GTT GCT GAT CCG ACA TCA AAG GTT CAT AAC TTC AAC AAT CTG1584
 281 Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu
 282 515 520 525
 284 TGG GTC GGC GGG AAT GGG TGC ATT CCA GAT GCG ACT GCC TGC AAC CCG1632
 285 Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro
 286 530 535 540
 288 ACT CGT ACG AGC GTC GCG TAT GCG CTC AAG GGT GCT GAG GCT GTA GTC1680
 289 Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val
 290 545 550 555 560
 293 AAT TAC CTT GGC GTC TCC TGA 1701
 294 Asn Tyr Leu Gly Val Ser *
 295 565
 298 (2) INFORMATION FOR SEQ ID NO: 3:
 300 (i) SEQUENCE CHARACTERISTICS:
 301 (A) LENGTH: 29
 302 (B) TYPE: amino acid
 303 (D) TOPOLOGY: linear
 305 (ii) MOLECULE TYPE: peptide
 307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 309 Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser
 310 1 5 10 15

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/911,969

DATE: 02/07/2002

TIME: 17:32:59

Input Set : N:\Crf3\RULE60\09911969.txt
Output Set: N:\CRF3\02072002\I911969.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:143 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:606 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:621 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20